

CRF Errors Corrected by the STIC Systems Branch

Sortal Number: 09/975,063

ENTERED

CRF Processing Date: 11/6/2001
 Edited by: [Signature]
 Verified by: [Signature] (STIC stat)

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 2/1/95

RAW SEQUENCE LISTING

DATE: 11/06/2001

PATENT APPLICATION: US/09/975,063

TIME: 08:01:49

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\11062001\I975063.raw

SEQUENCE LISTING

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4 (1) GENERAL INFORMATION:
6     (i) APPLICANT: POWELL, Jerry S.
8     (ii) TITLE OF INVENTION: HUMAN ERYTHROPOIETIN GENE: HIGH LEVEL
9         EXPRESSION IN STABLY TRANSFECTED MAMMALIAN CELLS
11    (iii) NUMBER OF SEQUENCES: 6
13    (iv) CORRESPONDENCE ADDRESS:
14        (A) ADDRESSEE: Dorsey & Whitney, LLP
15        (B) STREET: Suite 3400, 1420 Fifth Avenue, U.S. Bank Centre
16        (C) CITY: Seattle
17        (D) STATE: Washington
18        (E) COUNTRY: USA
19        (F) ZIP: 98101
21    (v) COMPUTER READABLE FORM:
22        (A) MEDIUM TYPE: Floppy disk
23        (B) COMPUTER: IBM PC compatible
24        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25        (D) SOFTWARE: WordPerfect 6/7/8
27    (vi) CURRENT APPLICATION DATA:
C--> 32        (A) APPLICATION NUMBER: US/09/975,063
C--> 33        (B) FILING DATE: 10-Oct-2001
35    (viii) ATTORNEY/AGENT INFORMATION:
36        (A) NAME: Roberts, Mark W..
37        (B) REGISTRATION NUMBER: 46,160
38        (C) REFERENCE/DOCKET NUMBER: 500582.03 (112893.109)
40    (ix) TELECOMMUNICATION INFORMATION:
41        (A) TELEPHONE: 206-903-8728
42        (B) TELEFAX: 206-903-8820
45 (2) INFORMATION FOR SEQ ID NO: 1:
47     (i) SEQUENCE CHARACTERISTICS:
48         (A) LENGTH: 2426 base pairs
49         (B) TYPE: nucleic acid
50         (C) STRANDEDNESS: single
51         (D) TOPOLOGY: linear
53     (ii) MOLECULE TYPE: DNA (genomic)
58     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
60 CCCGGTGTGG TCACCCGGCG CGCCCCAGGT CGCTGAGGGA CCCC GCCAG GCGCGGAGAT      60
62 GGGGGTGCAC GGTGAGTACT CGCGGGCTGG GCGCTCCCGC CCGCCCGGGT CCCTGTTTGA      120
64 GCGGGGATTT AGCGCCCCGG CTATTGGCCA GGAGGTGGCT GGGTTCAAGG ACCGGCGACT      180
66 TGTCAAGGAC CCCGGAAGGG GGAGGGGGGT GGGGCAGCCT CCACGTGCCA GCGGGGACTT      240
68 GGGGGAGTCC TTGGGGATGG CAAAAACCTG ACCTGTGAAG GGGACACAGT TTGGGGGTTG      300
70 AGGGGAAGAA GGTTTGGGGG GTTCTGCTGT GCCAGTGGAG AGGAAGCTGA TAAGCTGATA      360
72 ACCTGGGCGC TGGAGCCACC ACTTATCTGC CAGAGGGGAA GCCTCTGTCA CACCAGGATT      420
74 GAAGTTTGGC CGGAGAAGTG GATGCTGGTA GCCTGGGGGT GGGGTGTGCA CACGGCAGCA      480
76 GGATTGAATG AAGGCCAGGG AGGCAGCACC TGAGTGCTTG CATGGTTGGG GACAGGAAGG      540
78 ACGAGCTGGG GCAGAGACGT GGGGATGAAG GAAGCTGTCC TTCCACAGCC ACCCTTCTCC      600
80 CTCCCCGCTT GACTCTCAGC CTGGCTATCT GTTCTAGAAT GTCCTGCCTG GCTGTGGCTT      660

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82 CTCCTGTCCC TGCTGTGCGT CCCTCTGGGC CTCCCAGTCC TGGGCGCCCC ACCACGCCTC 720
84 ATCTGTGACA GCCGAGTCCT GCAGAGGTAC CTCTTGGAGG CCAAGAAGGC CGAGAATATC 780
86 ACGGTGAGAC CCCTTCCCCA GCACATTCCA CAGAACTCAC GCTCAGGGCT TCAGGGAAC 840
88 CCTCCCAGAT CCAGGAACCT GGCACCTGGT TTGGGGTGA GTTGGGAAGC TAGACACTGC 900
90 CCCCTACAT AAGAATAAGT CTGGTGGCCC CAAACCATAC CTGGAACTA GGCAAGGAGC 960
92 AAAGCCAGCA GATCCTACGC CTGTGGCCAG GGCCAGAGCC TTCAGGGACC CTTGACTCCC 1020
94 CGGGCTGTGT GCATTTTACA CGGGCTGTGC TGAACACTGC AGCTTGAATG AGAATATCAC 1080
96 TGTCCAGAC ACCAAAGTTA ATTTCTATGC CTGGAAGAGG ATGGAGGTGA GTTCCTTTT 1140
98 TTTTTTTTTT CTTTTCTTTT GGAGAACTC ATTTGCGAGC CTGATTTTGG ATGAAAGGGA 1200
100 GAATGATCGA GGGAAAGGTA AAATGGAGCA GCAGAGATGA GGCTGCCTGG GCGCAGAGGC 1260
102 TCACGTCTAT AATCCCAGGC TGAGATGGCC GAGATGGGAG AATTGCTTGA GCCCGGAGT 1320
104 TTCAGACCAA CCTAGGAGC ATAGTGAGAT CCCCCTCTC TACAAACATT TAAAAAATT 1380
106 AGTCAGGTGA AGTGGTGCAT GGTGGTAGTC CCAGATATTT GGAAGGCTGA GGCGGGAGGA 1440
108 TCGCTGGAGC CCAGGAATTT GAGGCTGCAG TGAGCTGTGA TCACACCACT GAACTCCAGC 1500
110 CTCAGTGACA GAGTGAGGCC CTGTCTCAA AAAGAAAAGA AAAAAAGAAA ATAATGAGGG 1560
112 CTGTATGAA TACGTTTATT ATTCATTCAC TCACTCACTC ACTCATTCAT TCATTCAATC 1620
114 ATTCAACAAG TCTTATTGCA TACCTTCTGT TTGCTCAGCT TGGTGCTTGG GGCTGCTGAG 1680
116 GGCAGGAGG GAGAGGGTGA CATCCCTCAG CTGACTCCCA GAGTCCACTC CCTGTAGGTC 1740
118 GGCAGCAGG CCGTAGAAGT CTGGCAGGGC CTGGCCCTGC TGTGGAAGC TGTCTGCGG 1800
120 GGCCAGGCCC TGTTGGTGAA CTCTTCCCAG CCGTGGGAGC CCCTGCAGCT GCATGTGGAT 1860
122 AAAGCCGTCA GTGGCCTTCG CAGCCTCACC ACTCTGCTTC GGGCTCTGGG AGCCAGGTG 1920
124 AGTAGGAGCG GACACTTCTG CTTGCCCTTT CTGTAAGAAG GGGAGAAGGG TCTTGCTAAG 1980
126 GAGTACAGGA ACTGTCCGTA TTCTTCCCT TTCTGTGGCA CTGCAGCGAC CTCCTGTTTC 2040
128 CTCCTTGGCA GAAGGAAGCC ATCTCCCTC CAGATGCGGC CTCAGCTGCT CCACTCCGAA 2100
130 CAATCACTGC TGACACTTTC CGCAAACCT TCCGAGTCTA CTCCAATTTT CTCGGGGGAA 2160
132 AGCTGAAGCT GTACACAGGG GAGGCCTGCA GGACAGGGGA CAGATGACCA GGTGTGTCCA 2220
134 CTGGGCATA TCCACACCT CCCTCACC AAATTGCTGT GCCACACCT CCCCGCCAC 2280
136 TCCTGAACCC CGTCAGGGG CTCTCAGCTC AGCGCCAGCC TGTCCCATGG ACACTCCAGT 2340
138 GCCACCAATG ACATCTCAGG GGCCAGAGGA ACTGTCCAGA GAGCAACTCT GAGATCTAAG 2400
140 GATGTACAG GGCCAACTTG AGGGCC 2426
142 (2) INFORMATION FOR SEQ ID NO: 2:
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 30 amino acids
146 (B) TYPE: amino acid
147 (C) STRANDEDNESS: single
148 (D) TOPOLOGY: linear
150 (ii) MOLECULE TYPE: peptide
155 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
W--> 157 Ala Pro Xaa Arg Leu Ile Leu Asp Ser Arg Val Leu Glu Arg Tyr Leu
158 1 5 10 15
W--> 160 Leu Glu Ala Lys Glu Ala Glu Xaa Ile Thr Asp Gly Gly Ala
161 20 25 30
163 (2) INFORMATION FOR SEQ ID NO: 3:
165 (i) SEQUENCE CHARACTERISTICS:
166 (A) LENGTH: 7 amino acids
167 (B) TYPE: amino acid
168 (C) STRANDEDNESS: single
169 (D) TOPOLOGY: linear
171 (ii) MOLECULE TYPE: peptide

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176 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
178 Glu Ala Lys Glu Ala Glu Asn
179 1 5

181 (2) INFORMATION FOR SEQ ID NO: 4:
183 (i) SEQUENCE CHARACTERISTICS:
184 (A) LENGTH: 20 base pairs
185 (B) TYPE: nucleic acid
186 (C) STRANDEDNESS: single
187 (D) TOPOLOGY: linear
189 (ii) MOLECULE TYPE: DNA (genomic)

194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
196 TTYTCDGCTT CYTTDGCTTC 20

198 (2) INFORMATION FOR SEQ ID NO: 5:
200 (i) SEQUENCE CHARACTERISTICS:
201 (A) LENGTH: 6 amino acids
202 (B) TYPE: amino acid
203 (C) STRANDEDNESS: single
204 (D) TOPOLOGY: linear
206 (ii) MOLECULE TYPE: peptide

211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
213 Glu Asn Ile Thr Asp Gly
214 1 5

216 (2) INFORMATION FOR SEQ ID NO: 6:
218 (i) SEQUENCE CHARACTERISTICS:
219 (A) LENGTH: 23 base pairs
220 (B) TYPE: nucleic acid
221 (C) STRANDEDNESS: single
222 (D) TOPOLOGY: linear
224 (ii) MOLECULE TYPE: DNA (genomic)

229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
231 AGCTCCTCCA TCAGTATTAT TTY 23

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/975,063

DATE: 11/06/2001

TIME: 08:01:50

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\11062001\I975063.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2